

PAGE MSARVRSRSGRGDGO.EAPDVVAFVAPGE.SQOEEPPPT
|| || | | | : : | : : ||
GAGE2 MSWRGGRSTYRERPRRYVEPPMIGFMRPEQFSDEVEPAT
GAGE1 Y E M
GAGE3 K Y Q V
GAGE4 Y Q M
GAGES,6 Y Q V
|| || | : : | | : : | : : || : |
MAGES MSLEQKSQ.KPEEGUDTQE.EALGLVGVOAATTEEQEAVS
MAGES LG Y A QAG. P MD IPA KA

```
PAGE      DNQDIEPGQERE..... GTPPIERRKVEGDCQE  
          :: || :| |         |   : | |    ||  
PAGE2     P.EEGEPATQRQDPAAAQEGEDEGCASAGQGPKPEAHSQE  
PAGE1                                  D  
PAGE3-6                                       D  
  
MAGES     SSSPLVVGTLGEVPAAGSPPGLK.SPQGASAIPTAIDFTLW  
PAGE8      T IM E TDS SP QO E SSL VT S
```

```

PAGE          MDLEKTRSERGDGSUVKERTPNPNKHAKTKEAGDGQP
              : | | | | : | : | | | | | : |
GAGE2         QGHPQTGCCECDGPDGQEMDPNPNPEEVKTPPEEGEKQSQC
GAGE1         M . MR HYVA..
GAGE3-5       M
GAGE6         V
              : | | : | : | | | | : |
MAGE5         RQSIKGSSNQEEEGPSTSPDP...ESVFRAALSKKVADLIHFLLLKY
MAGE8         S DE SN AHL L E DE E VR R..

```

```
PAGE1      MSA...RVRSRSRGRGDQGEAPDVVAFVAPGES.....
           ||.  |.|||.|.:.||::|||...:|...|.
PAGE2      MSELVVRARSQSSSRGNDQESSQPVGSGVIVQEPTEZKR
           .....
PAGE3      .....MTSF
```

```
PAGE1 QEEPPTDNQGPD.....MEAFQOEL
      |:|||||: : :|||!
PAGE2 QEEPPTDNQDIEPGQEREGTPPIERKVEGDCQEM
      : ||: | |||: : :|!
PAGE3 NKTAPPIESQDYTPGQERDEGALDFQVPSLAAXWEL
```

```
PAGE1 DLEKTRSERGDSGVKEKTPPNPKHAXTKAAGDGQP  
      :| |: | |: | |: | |: | |: | |: | |: |  
PAGE2 ALLKTEDEPGDGPVREGIMPTFDLTKVLEAGDAQP  
      |||: |: |: |: |: |: |: |: |: |: |: |  
PAGE3 TRPKTGGERGDPNVKGESLPNLFVKIPEAGEGQPSV
```


Replacement Sheets

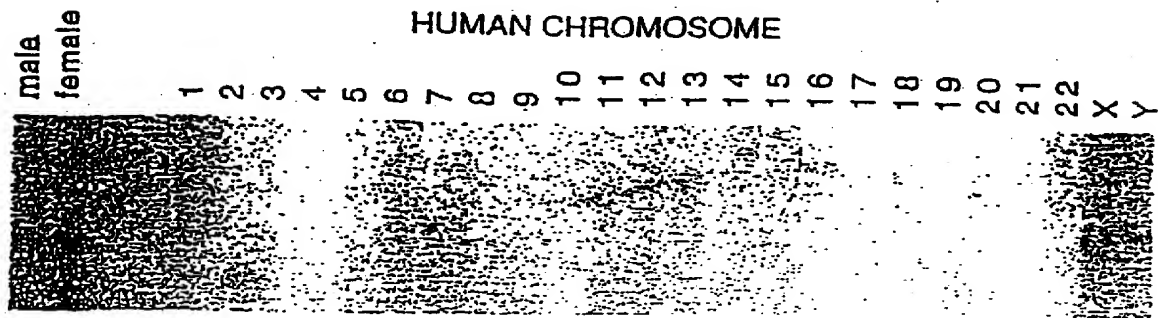


FIG. 2C

Replacement Sheets

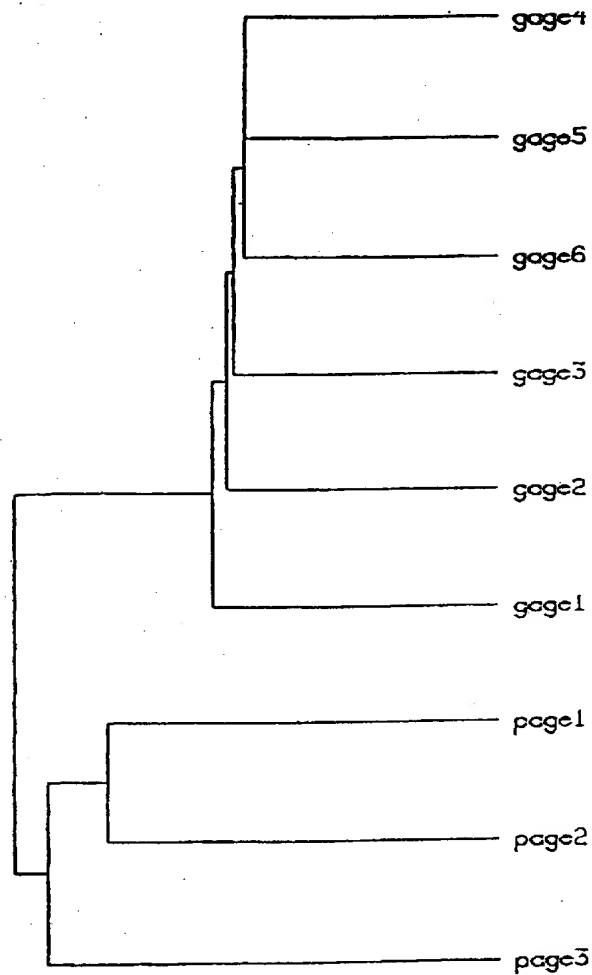


FIG. 3

Replacement Sheets

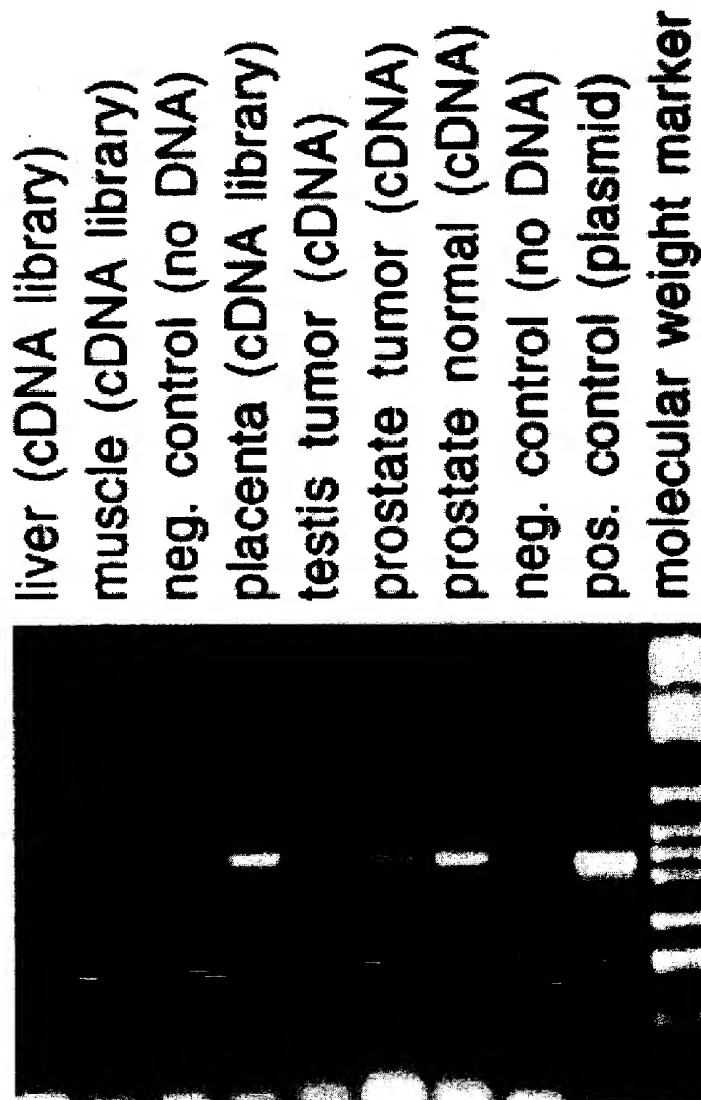


FIG. 4

Replacement Sheets

Page 4 sequence (bold and underline: open reading frame).

GAAGAATTCGCCAGGCTCTCTGCTGACTCAAGTTCTTCAGTTCACGATCTTCTAGTT
GCAGCG

ATGAGTGCACGAGTGAGATCAAGATCCAGAGGAAGAGGAGATGGTCAGGAGGCTCCC
GATGTGGTTGCATTTCGTGGCTCCCGGTGAATCTCAGCAAGAGGAACCACTGAC
AATCAGGATATTGAACCTGGACAAGAGAGAGAAGGAACACCTCCGATCGAAGAACGT
AAAGTAGAAGGTGATTGCCAGGAAATGGATCTGGAAAAGACTCGGAGTGAGCGTGGA
GATGGCTCTGATGTAAAAGAGAAGACTCCACCTAATCCTAAGCATGCTAAGACTAAA
GAAGCAGGAGATGGGCAGCCA

TAAGTTAAAAAGAAGACAAGCTGAAGCTACACACATGGCTGATGTCACATT
GAAAATGTGACTGAAAATTTGAAAATTTCTCTCAATAAAGTTTGAGTTTTCTCTGAA

FIG. 5